FIGURE 1

```
   1  ATGTCAGTGGGAGCCATGAAGAAGGGAGTGGGGAGGGCAGTTGGGCTTGGAGGCGGCAGC   60
  61  GGCTGCCAGGCTACGGAGGAAGACCCCCTTCCCGACTGCGGGGCTTGCGCTCCGGGACAA  120
 121  GGTGGCAGGCGCTGGAGGCTGCCGCAGCCTGCGTGGGTGGAGGGGAGCTCAGCTCGGTTG  180
 181  TGGGAGCAGGCGACCGGCACTGGCTGGATGGACCTGGAAGCCTCGCTGCTGCCCACTGGT  240
 241  CCCAATGCCAGCAACACCTCTGATGGCCCCGATAACCTCACTTCAGCAGGATCACCTCCT  300
 301  CGCACGGGGAGCATCTCCTACATCAACATCATCATGCCTTCGGTGTTCGGCACCATCTGC  360
 361  CTCCTGGGCATCATCGGGAACTCCACGGTCATCTTCGCGGTCGTGAAGAAGTCCAAGCTG  420
 421  CACTGGTGCAACAACGTCCCCGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCCTC  480
 481  TTTCTCCTGGGCATGCCCTTCATGATCCACCAGCTCATGGGCAATGGGGTGTGGCACTTT  540
 541  GGGGAGACCATGTGCACCCTCATCACGGCCATGGATGCCAATAGTCAGTTCACCAGCACC  600
 601  TACATCCTGACCGCCATGGCCATTGACCGCTACCTGGCCACTGTCCACCCCATCTCTTCC  660
 661  ACGAAGTTCCGGAAGCCCTCTGTGGCCACCCTGGTGATCTGCCTCCTGTGGGCCCTCTCC  720
 721  TTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCCTTCCCAGGAGGTGCA  780
 781  GTGGGCTGCGGCATACGCCTGCCCAACCCAGACACTGACCTCTACTGGTTCACCCTGTAC  840
 841  CAGTTTTTCCTGGCCTTTGCCCTGCCTTTTGTGGTCATCACAGCCGCATACGTGAGGATC  900
 901  CTGCAGCGCATGACGTCCTCAGTGGCCCCCGCCTCCCAGCGCAGCATCCGGCTGCGGACA  960
 961  AAGAGGGTGACCCGCACAGCCATCGCCATCTGTCTGGTCTTCTTTGTGTGCTGGGCACCC 1020
1021  TACTATGTGCTACAGCTGACCCAGTTGTCCATCAGCCGCCCGACCCTCACCTTTGTCTAC 1080
1081  TTATACAATGCGGCCATCAGCTTGGGCTATGCCAACAGCTGCCTCAACCCCTTTGTGTAC 1140
1141  ATCGTGCTCTGTGAGACGTTCCGCAAACGCTTGGTCCTGTCGGTGAAGCCTGCAGCCCAG 1200
1201  GGGCAGCTTCGCGCTGTCAGCAACGCTCAGACGGCTGACGAGGAGAGGACAGAAAGCAAA 1260
1261  GGCACCTGA                                                     1269
```

FIGURE 2

```
  1  M S V G A M K K G V G R A V G L G G G S  20
 21  G C Q A T E E D P L P D C G A C A P G Q  40
 41  G G R R W R L P Q P A W V E G S S A R L  60
 61  W E Q A T G T G W M D L E A S L L P T G  80
 81  P N A S N T S D G P D N L T S A G S P P  100
101  R T G S I S Y I N I I M P S V F G T I C  120
121  L L G I I G N S T V I F A V V K K S K L  140
141  H W C N N V P D I F I I N L S V V D L L  160
161  F L L G M P F M I H Q L M G N G V W H F  180
181  G E T M C T L I T A M D A N S Q F T S T  200
201  Y I L T A M A I D R Y L A T V H P I S S  220
221  T K F R K P S V A T L V I C L L W A L S  240
241  F I S I T P V W L Y A R L I P F P G G A  260
261  V G C G I R L P N P D T D L Y W F T L Y  280
281  Q F F L A F A L P F V V I T A A Y V R I  300
301  L Q R M T S S V A P A S Q R S I R L R T  320
321  K R V T R T A I A I C L V F F V C W A P  340
341  Y Y V L Q L T Q L S I S R P T L T F V Y  360
361  L Y N A A I S L G Y A N S C L N P F V Y  380
381  I V L C E T F R K R L V L S V K P A A Q  400
401  G Q L R A V S N A Q T A D E E R T E S K  420
421  G T                                    422
```

FIGURE 3

```
  1  M S V G A M K K G V G R A V G L G G G S  20

 21  G C Q A T E E D P L P D C G A C A P G Q  40

 41  G G R R W R L P Q P A W V E G S S A R L  60

 61  W E Q A T G T G W M D L E A S L L P T G  80

 81  P N A S N T S D G P D N L T S A G S P P  100

101  R T G S I S Y I N I I M P S V F G T I C  120
         I
121  L L G I I G N S T V I F A V V K K S K L  140
                                   II
141  H W C N N V P D I F I I N L S V V D L L  160

161  F L L G M P F M I H Q L M G N G V W H F  180

181  G E T M C T L I T A M D A N S Q F T S T  200
        III
201  Y I L T A M A I D R Y L A T V H P I S S  220

221  T K F R K P S V A T L V I C L L W A L S  240
                          IV
241  F I S I T P V W L Y A R L I P F P G G A  260

261  V G C G I R L P N P D T D L Y W F T L Y  280
                    V

281  Q F F L A F A L P F V V I T A A Y V R I  300

301  L Q R M T S S V A P A S Q R S I R L R T  320
                                  VI
321  K R V T R T A I A I C L V F F V C W A P  340

341  Y Y V L Q L T Q L S I S R P T L T F V Y  360
                       VII
361  L Y N A A I S L G Y A N S C L N P F V Y  380

381  I V L C E T F R K R L V L S V K P A A Q  400

401  G Q L R A V S N A Q T A D E E R T E S K  420

421  G T                                     422
```

FIGURE 4

```
   1  GCAGGCGACCTGCACCGGCTGCATGGATCTGCAAACCTCGTTGCTGTCCACTGGCCCCAA   60
  61  TGCCAGCAACATCTCCGATGGCCAGGATAATCTCACATTGCCGGGGTCACCTCCTCGCAC  120
 121  AGGGAGTGTCTCCTACATCAACATCATTATGCCTTCCGTGTTTGGTACCATCTGTCTCCT  180
 181  GGGCATCGTGGGAAACTCCACGGTCATCTTTGCTGTGGTGAAGAAGTCCAAGCTACACTG  240
 241  GTGCAGCAACGTCCCCGACATCTTCATCATCAACCTCTCTGTGGTGGATCTGCTCTTCCT  300
 301  GCTGGGCATGCCTTTCATGATCCACCAGCTCATGGGGAACGGCGTCTGGCACTTTGGGGA  360
 361  AACCATGTGCACCCTCATCACAGCCATGGACGCCAACAGTCAGTTCACTAGCACCTACAT  420
 421  CCTGACTGCCATGACCATTGACCGCTACTTGGCCACCGTCCACCCCATCTCCTCCACCAA  480
 481  GTTCCGGAAGCCCTCCATGGCCACCCTGGTGATCTGCCTCCTGTGGGCGCTCTCCTTCAT  540
 541  CAGTATCACCCCTGTGTGGCTCTACGCCAGGCTCATTCCCTTCCCAGGGGGTGCTGTGGG  600
 601  CTGTGGCATCCGCCTGCCAAACCCGGACACTGACCTCTACTGGTTCACTCTGTACCAGTT  660
 661  TTTCCTGGCCTTTGCCCTTCCGTTTGTGGTCATTACCGCCGCATACGTGAAAATACTACA  720
 721  GCGCATGACGTCTTCGGTGGCCCCAGCCTCCCAACGCAGCATCCGGCTTCGGACAAAGAG  780
 781  GGTGACCCGCACGGCCATTGCCATCTGTCTGGTCTTCTTTGTGTGCTGGGCACCCTACTA  840
 841  TGTGCTGCAGCTGACCCAGCTGTCCATCAGCCGCCCGACCCTCACGTTTGTCTACTTGTA  900
 901  CAACGCGGCCATCAGCTTGGGCTATGCTAACAGCTGCCTGAACCCCTTTGTGTACATAGT  960
 961  GCTCTGTGAGACCTTTCGAAAACGCTTGGTGTTGTCAGTGAAGCCTGCAGCCCAGGGGCA 1020
1021  GCTCCGCACGGTCAGCAACGCTCAGACAGCTGATGAGGAGAGGACAGAAAGCAAAGGCAC 1080
1081  CTGACAATTCCCCAGTCGCCTCCAAGTCAGGCCACCCCATCAAACCGTGGGGAGAGATAC 1140
1141  TGAGATTAAACCCAAGGCTACCCTGGGAGAATGCAGAGGCTGGAGGCTGGGGGCTTGTAG 1200
1201  CAACCACATTCCAC                                                1214
```

FIGURE 5

```
  1  M D L Q T S L L S T G P N A S N I S D G   20
 21  Q D N L T L P G S P P R T G S V S Y I N   40
 41  I I M P S V F G T I C L L G I V G N S T   60
 61  V I F A V V K K S K L H W C S N V P D I   80
 81  F I I N L S V V D L L F L L G M P F M I  100
101  H Q L M G N G V W H F G E T M C T L I T  120
121  A M D A N S Q F T S T Y I L T A M T I D  140
141  R Y L A T V H P I S S T K F R K P S M A  160
161  T L V I C L L W A L S F I S I T P V W L  180
181  Y A R L I P F P G G A V G C G I R L P N  200
201  P D T D L Y W F T L Y Q F F L A F A L P  220
221  F V V I T A A Y V K I L Q R M T S S V A  240
241  P A S Q R S I R L R T K R V T R T A I A  260
261  I C L V F F V C W A P Y Y V L Q L T Q L  280
281  S I S R P T L T F V Y L Y N A A I S L G  300
301  Y A N S C L N P F V Y I V L C E T F R K  320
321  R L V L S V K P A A Q G Q L R T V S N A  340
341  Q T A D E E R T E S K G T *             354
```

FIGURE 6

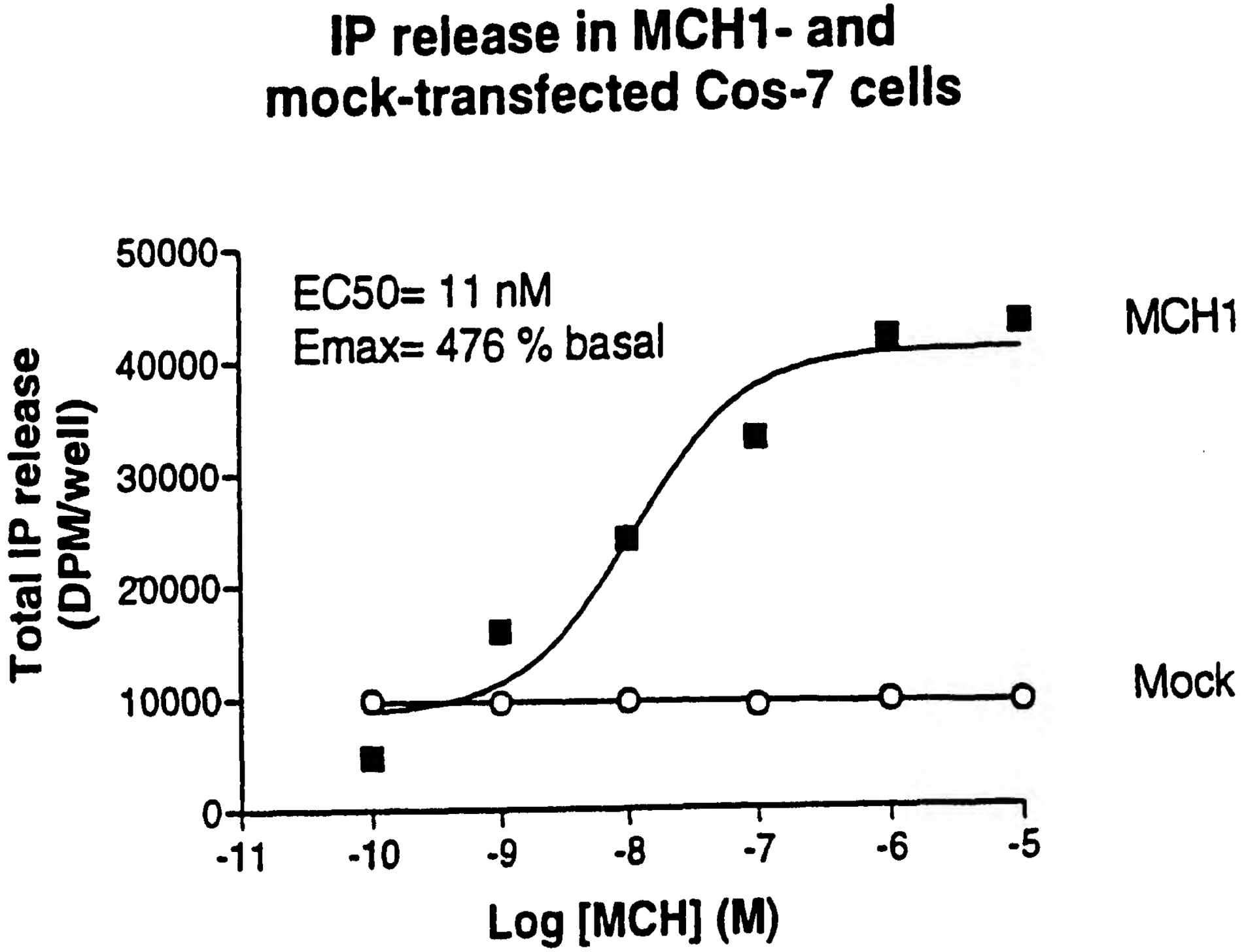
IP release in MCH1- and mock-transfected Cos-7 cells
EC50= 11 nM
Emax= 476 % basal
MCH1
Mock
Total IP release (DPM/well)
50000
40000
30000
20000
10000
0
-11
-10
-9
-8
-7
-6
-5
Log [MCH] (M)

FIGURE 7A

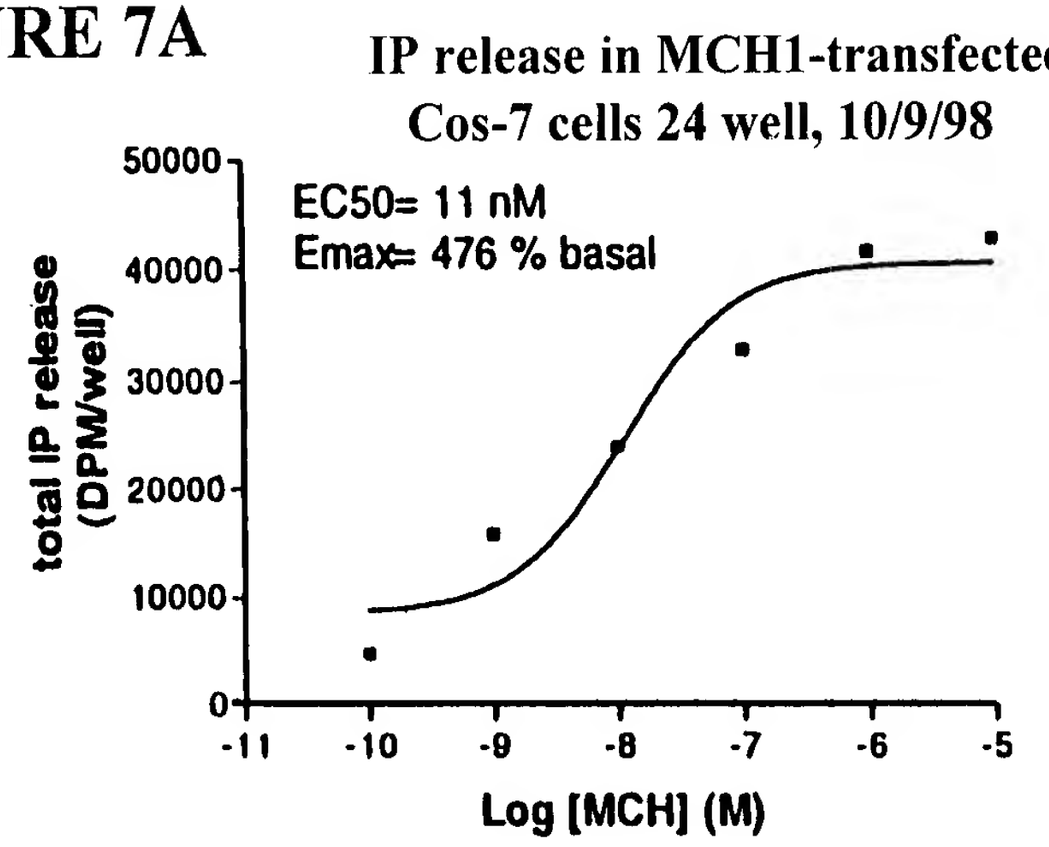

FIGURE 7B

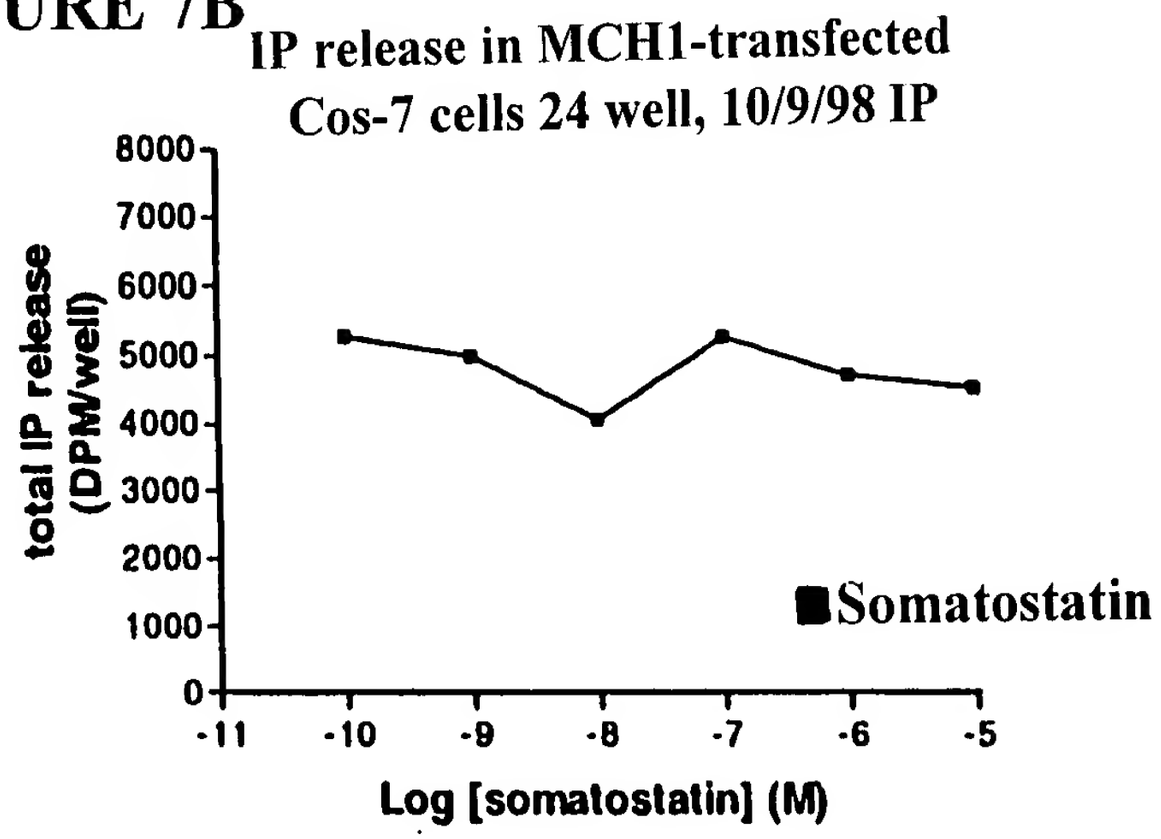

FIGURE 7C

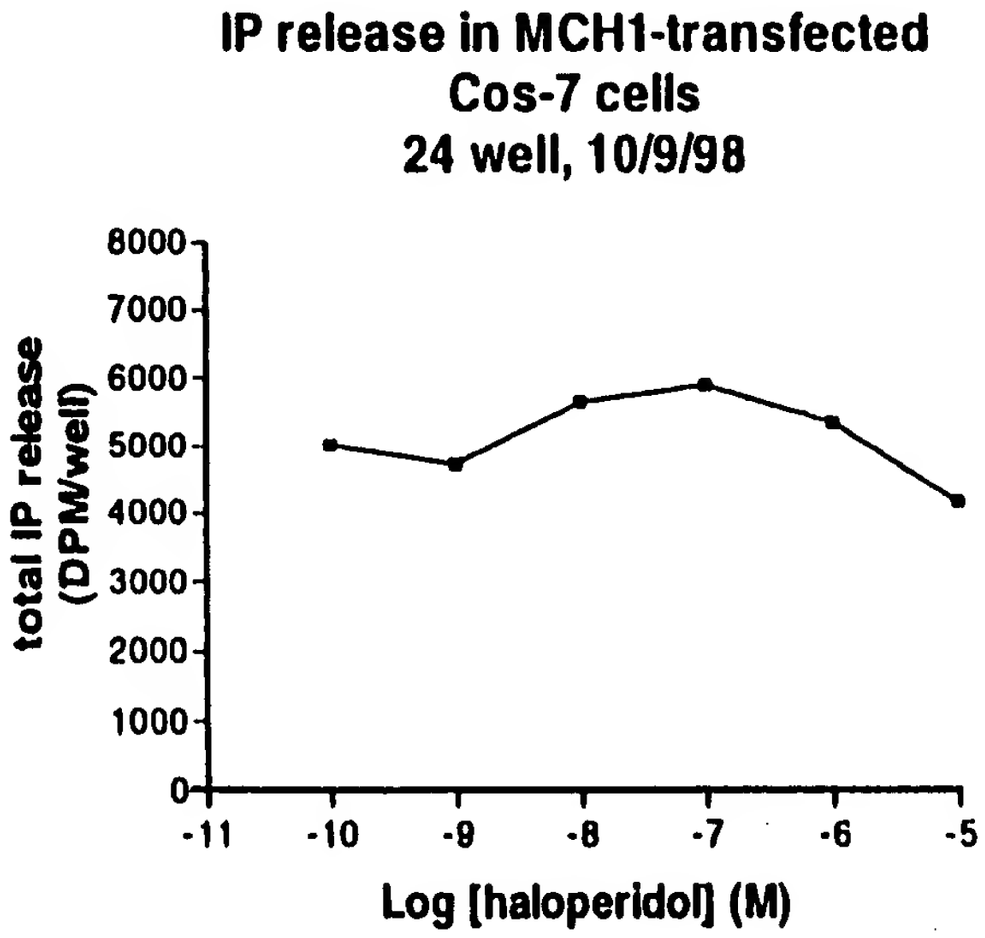

FIGURE 7D

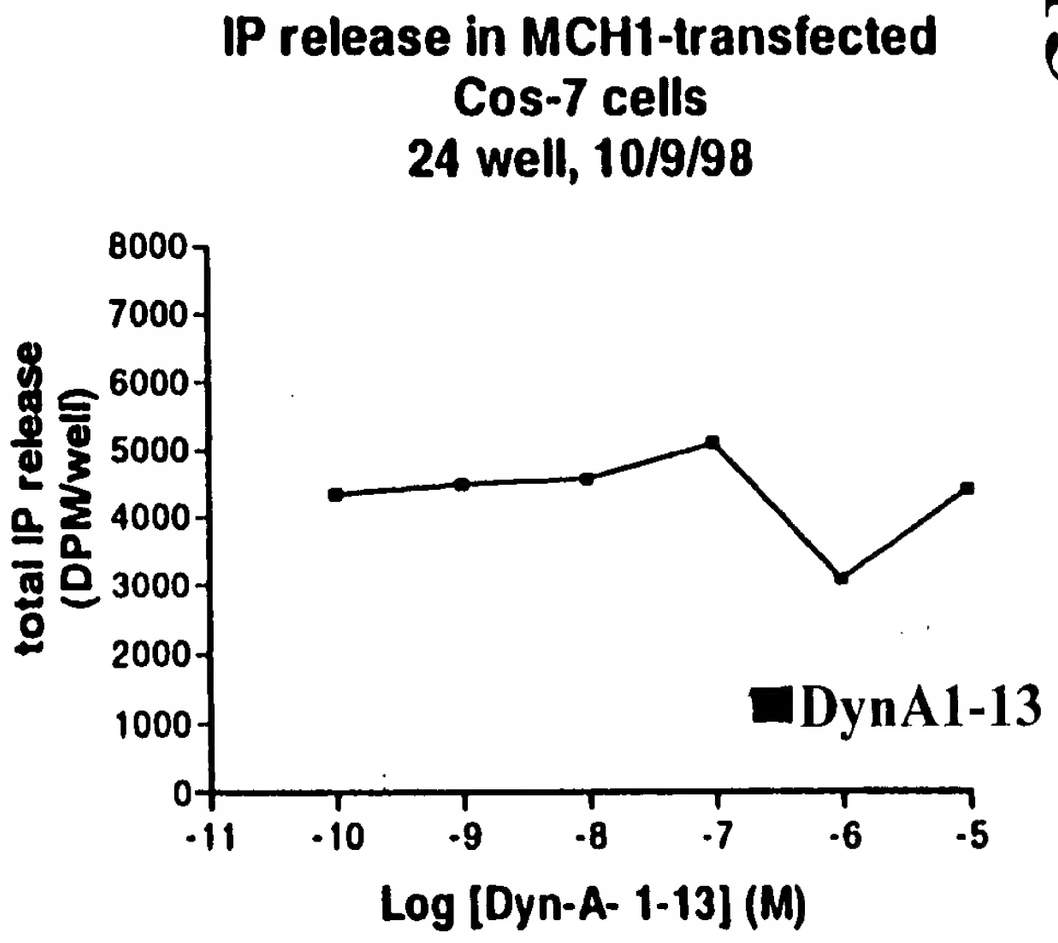

FIGURE 8A

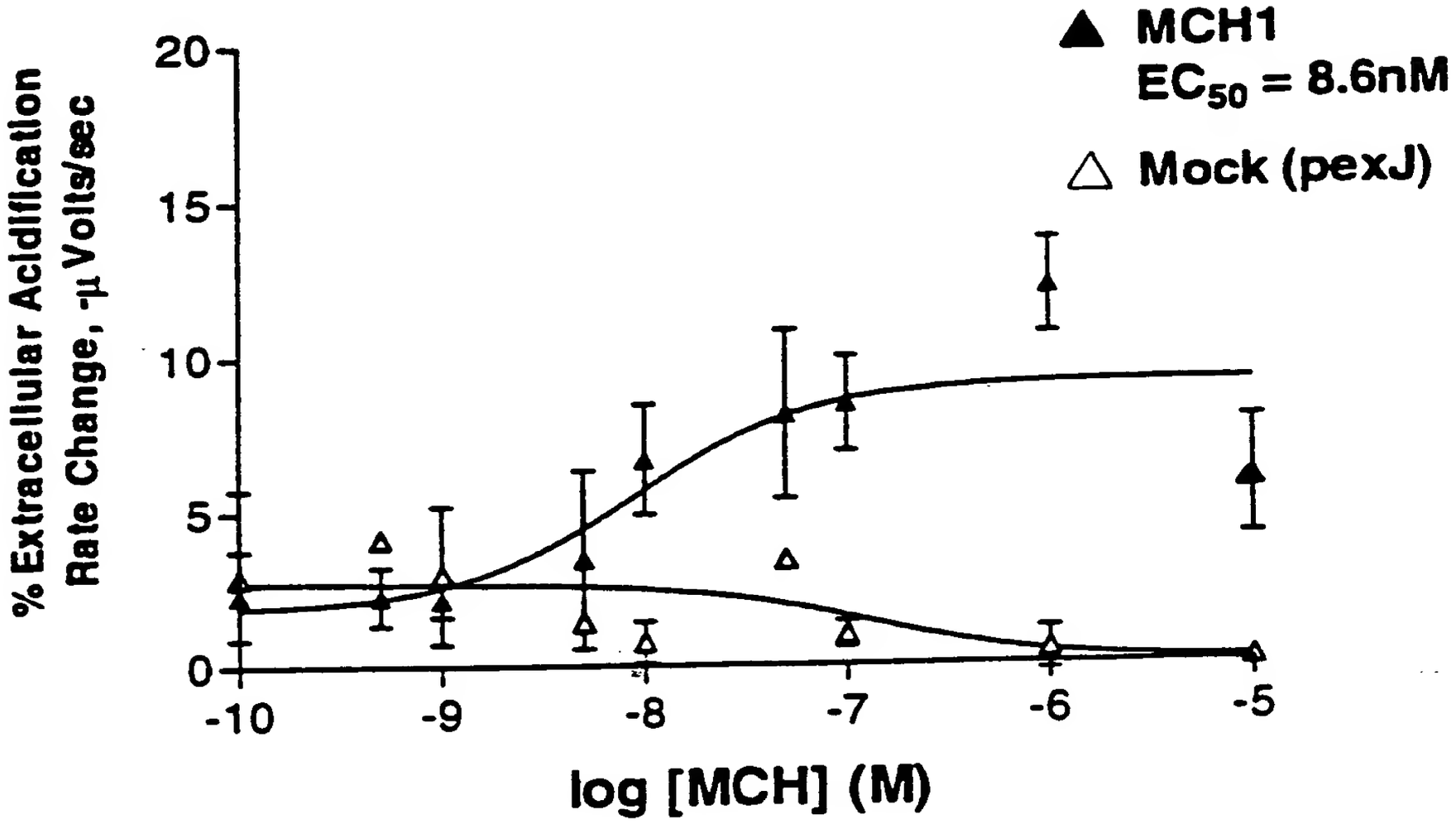

FIGURE 8B

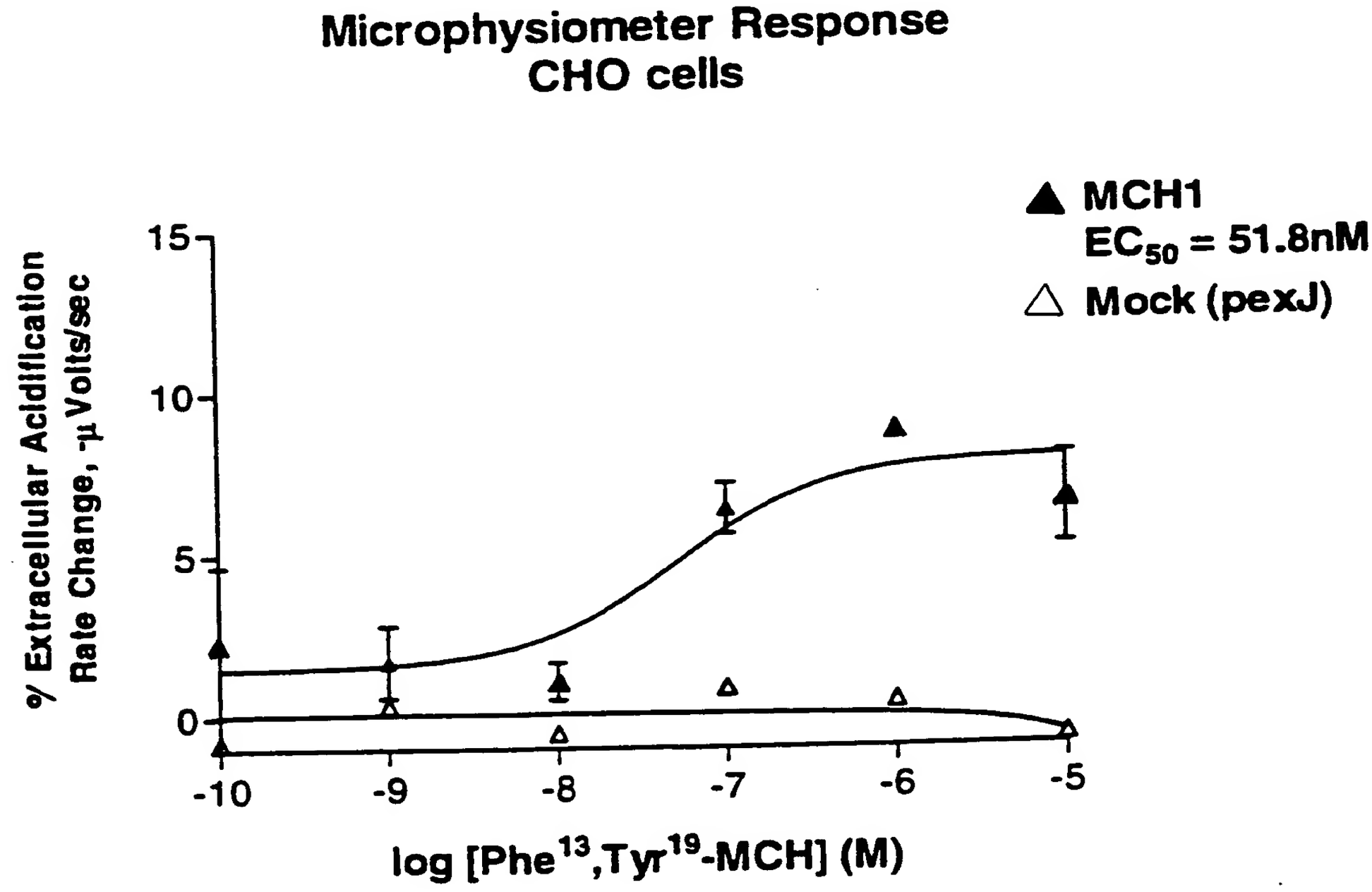

FIGURE 9

Agonist-Mediated c-fos-β-gal Activity in Cos-7 Cells

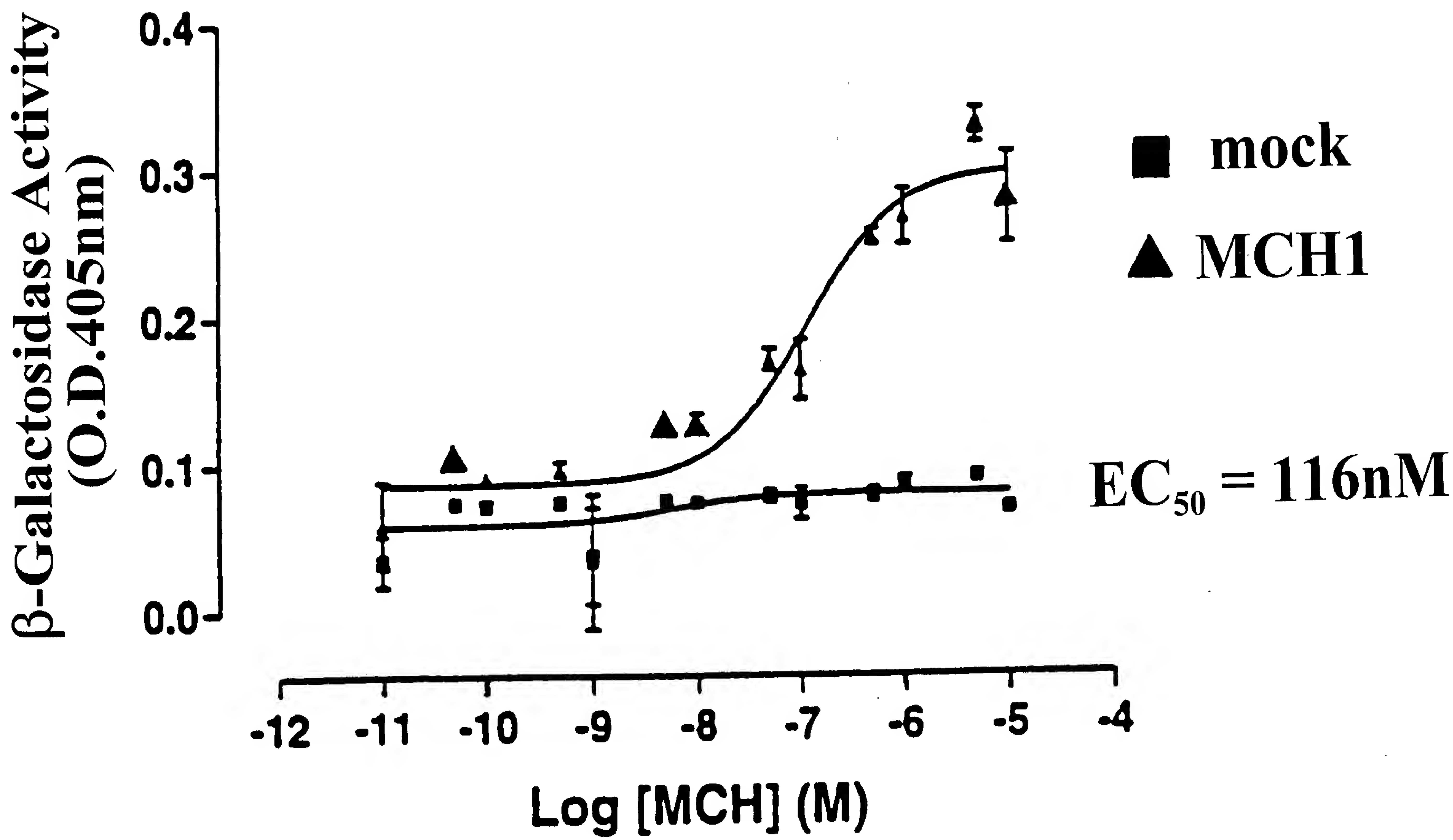

FIGURE 10A

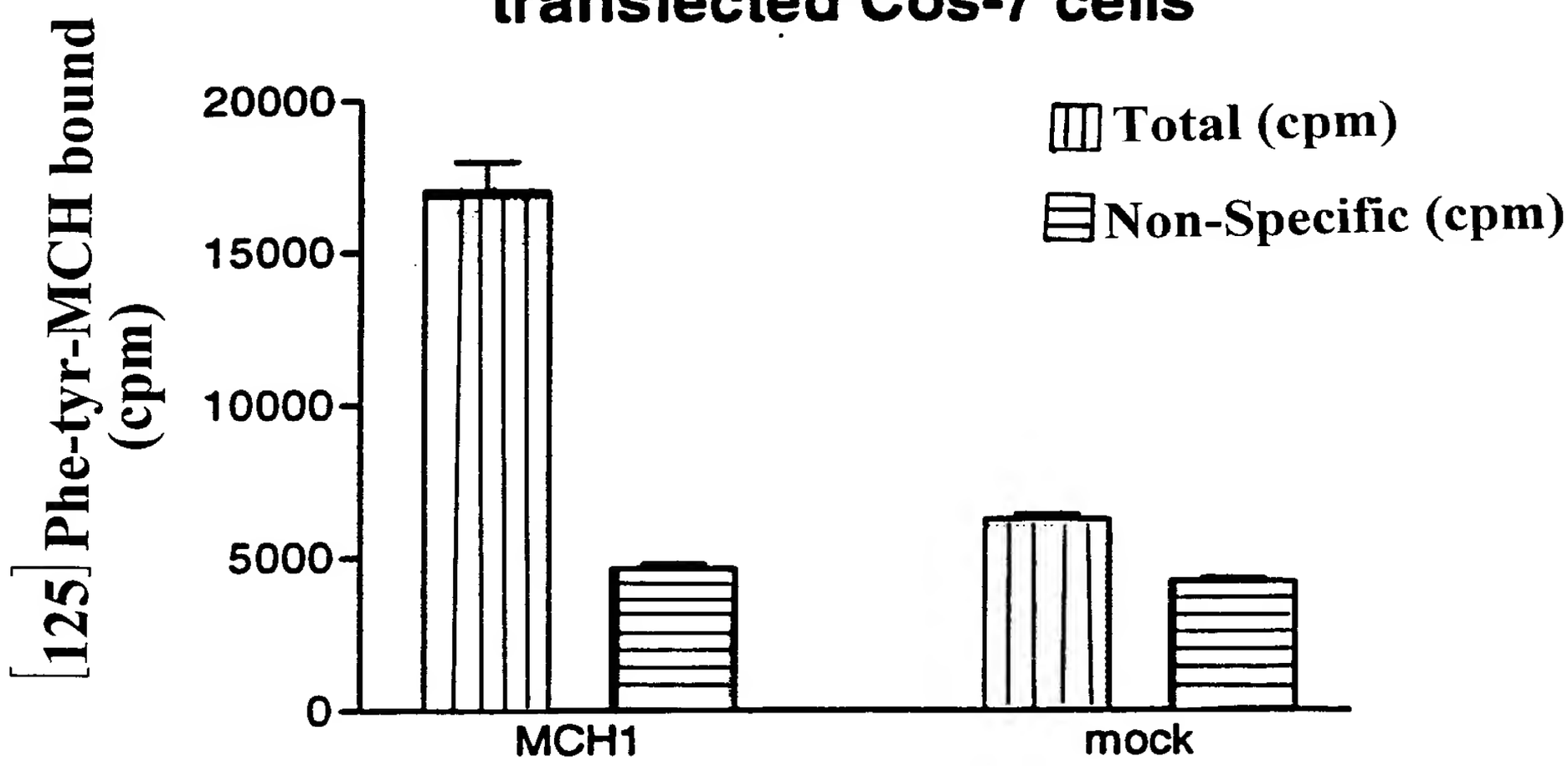

FIGURE 10B

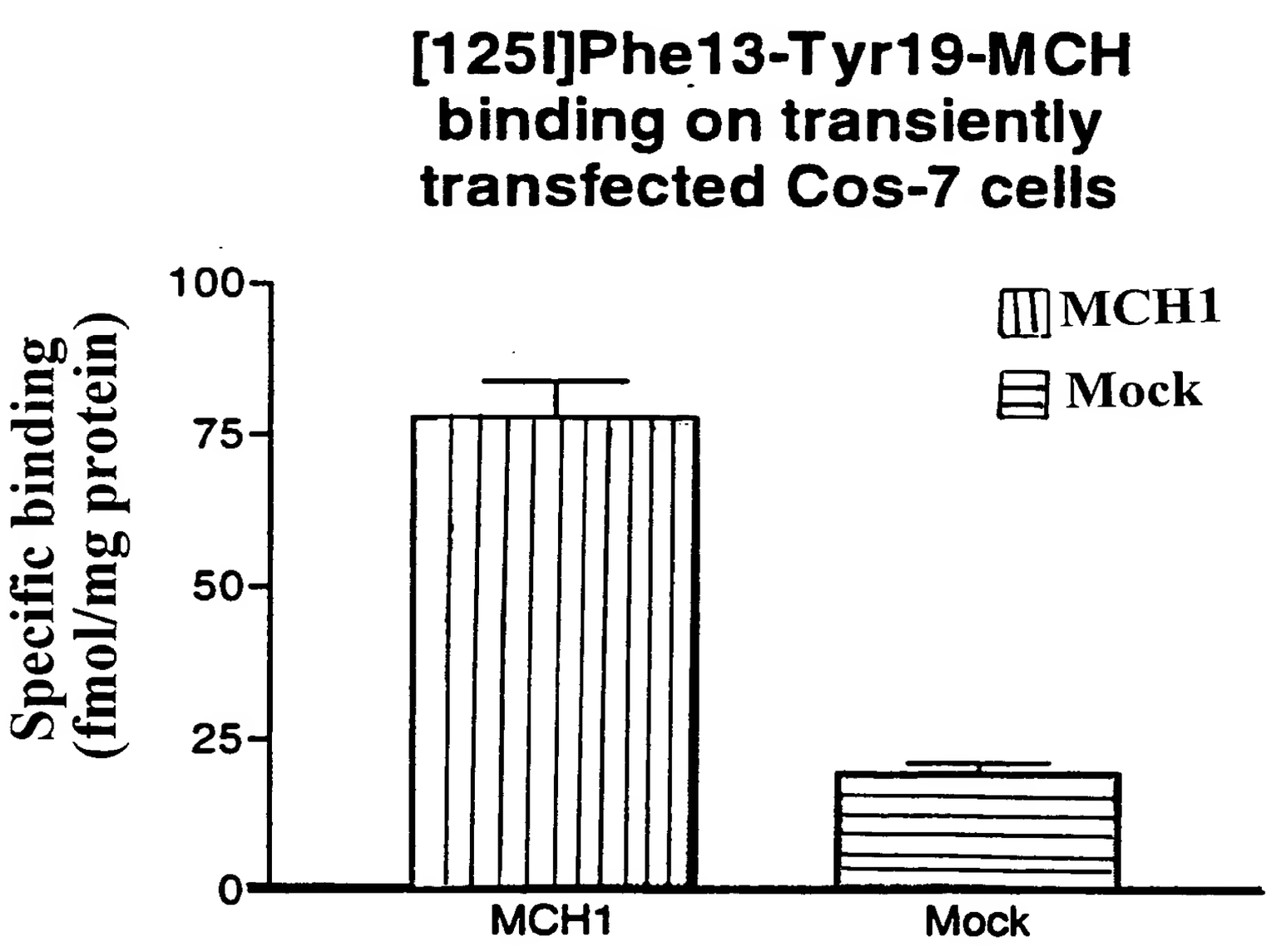

FIGURE 11

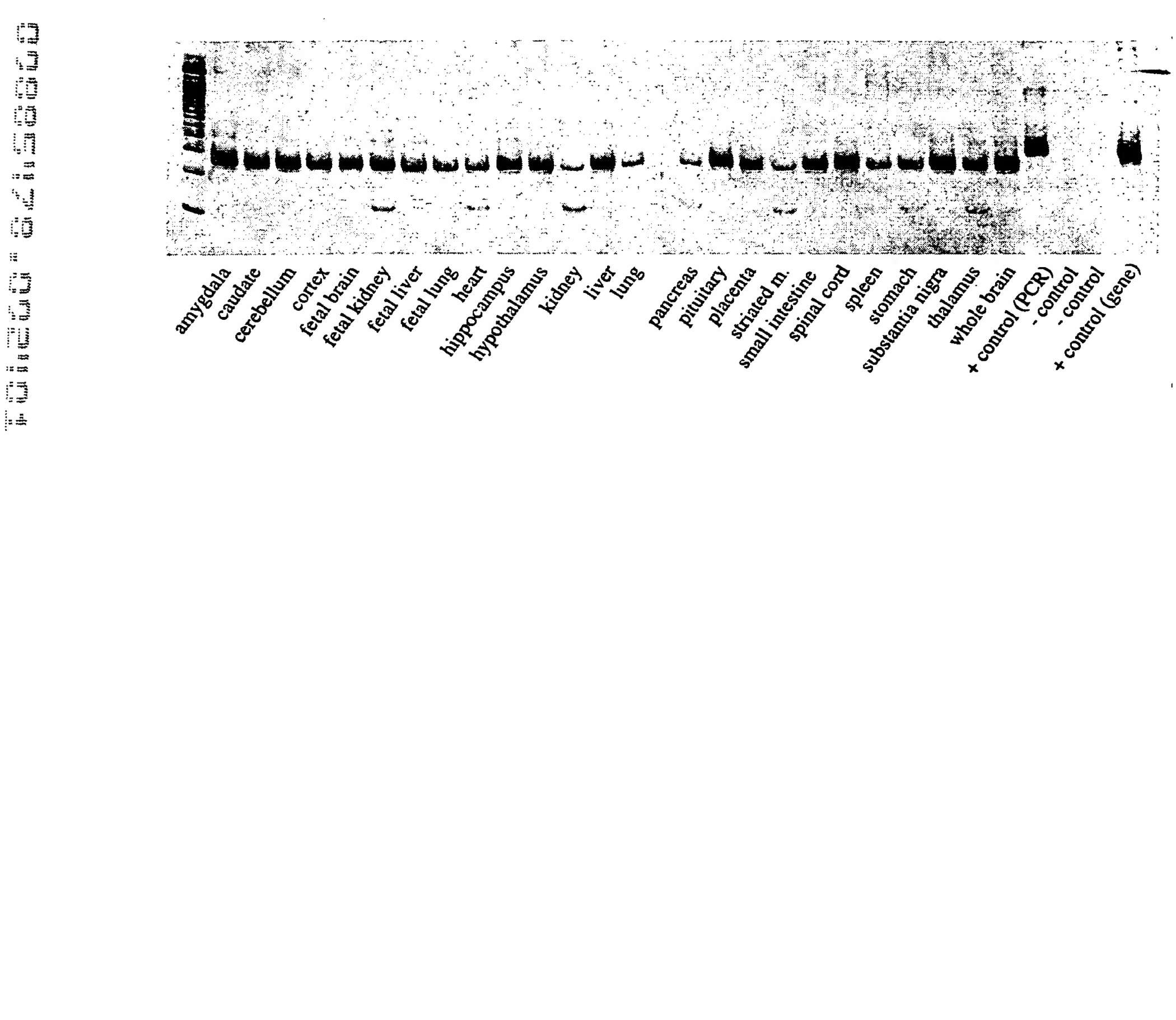
amygdala
caudate
cerebellum
cortex
fetal brain
fetal kidney
fetal liver
fetal lung
heart
hippocampus
hypothalamus
kidney
liver
lung
pancreas
pituitary
placenta
striated m.
small intestine
spinal cord
spleen
stomach
substantia nigra
thalamus
whole brain
+ control (PCR)
- control
- control
+ control (gene)

FIGURE 12

```
                1                                                   40
TL231           MSVGAMKKGV  GRAVGLGGGS  GCQATEEDPL  PDCGACAPGQ
R106            MSVGAMKKGV  GRAVGLGGGS  GCQATEEDPL  PDCGACAPGQ
R114            MSVGAaKKGV  GRAVGLGGGS  GCQATEEDPL  PDCGACAPGQ
BO120           ~~~~~~~~~~  ~~~~~~~~~~  ~~~~~~~~~~  ~~~~~~~~~~

               41                                                   80
TL231           GGRRWRLPQP  AWVEGSSARL  WEQATGTGWM  DLEASLLPTG
R106            GGRRWRLPQP  AWVEGSSARL  WEQATGTGWa  DLEASLLPTG
R114            GGRRWRLPQP  AWVEGSSARL  WEQATGTGWa  DLEASLLPTG
BO120           ~~~~~~~~~~  ~~~~~~~~~~  ~~~~~~~~~~M  DLEASLLPTG

                81                    100
TL231           PNASNTSDGP  DNLTSAGSPP...
R106            PNASNTSDGP  DNLTSAGSPP...
R114            PNASNTSDGP  DNLTSAGSPP...
BO120           PNASNTSDGP  DNLTSAGSPP...
```

FIGURE 13

```
  1  M S V G A M K K G V G R A V G L G G G S  20
 21  G C Q A T E E D P L P D C G A C A P G Q  40
 41  G G R R W R L P Q P A W V E G S S A R L  60
 61  W E Q A T G T G W A D L E A S L L P T G  80
 81  P N A S N T S D G P D N L T S A G S P P  100
101  R T G S I S Y I N I I M P S V F G T I C  120
121  L L G I I G N S T V I F A V V K K S K L  140
141  H W C N N V P D I F I I N L S V V D L L  160
161  F L L G M P F M I H Q L M G N G V W H F  180
181  G E T M C T L I T A M D A N S Q F T S T  200
201  Y I L T A M A I D R Y L A T V H P I S S  220
221  T K F R K P S V A T L V I C L L W A L S  240
241  F I S I T P V W L Y A R L I P F P G G A  260
261  V G C G I R L P N P D T D L Y W F T L Y  280
281  Q F F L A F A L P F V V I T A A Y V R I  300
301  L Q R M T S S V A P A S Q R S I R L R T  320
321  K R V T R T A I A I C L V F F V C W A P  340
341  Y Y V L Q L T Q L S I S R P T L T F V Y  360
361  L Y N A A I S L G Y A N S C L N P F V Y  380
381  I V L C E T F R K R L V L S V K P A A Q  400
401  G Q L R A V S N A Q T A D E E R T E S K  420
421  G T                                    422
```

FIGURE 14

```
  1  M S V G A A K K G V G R A V G L G G G S  20
 21  G C Q A T E E D P L P D C G A C A P G Q  40
 41  G G R R W R L P Q P A W V E G S S A R L  60
 61  W E Q A T G T G W A D L E A S L L P T G  80
 81  P N A S N T S D G P D N L T S A G S P P  100
101  R T G S I S Y I N I I M P S V F G T I C  120
121  L L G I I G N S T V I F A V V K K S K L  140
141  H W C N N V P D I F I I N L S V V D L L  160
161  F L L G M P F M I H Q L M G N G V W H F  180
181  G E T M C T L I T A M D A N S Q F T S T  200
201  Y I L T A M A I D R Y L A T V H P I S S  220
221  T K F R K P S V A T L V I C L L W A L S  240
241  F I S I T P V W L Y A R L I P F P G G A  260
261  V G C G I R L P N P D T D L Y W F T L Y  280
281  Q F F L A F A L P F V V I T A A Y V R I  300
301  L Q R M T S S V A P A S Q R S I R L R T  320
321  K R V T R T A I A I C L V F F V C W A P  340
341  Y Y V L Q L T Q L S I S R P T L T F V Y  360
361  L Y N A A I S L G Y A N S C L N P F V Y  380
381  I V L C E T F R K R L V L S V K P A A Q  400
401  G Q L R A V S N A Q T A D E E R T E S K  420
421  G T                                    422
```

FIGURE 15

```
  1  M D L E A S L L P T G P N A S N T S D G  20
 21  P D N L T S A G S P P R T G S I S Y I N  40
 41  I I M P S V F G T I C L L G I I G N S T  60
 61  V I F A V V K K S K L H W C N N V P D I  80
 81  F I I N L S V V D L L F L L G M P F M I  100
101  H Q L M G N G V W H F G E T M C T L I T  120
121  A M D A N S Q F T S T Y I L T A M A I D  140
141  R Y L A T V H P I S S T K F R K P S V A  160
161  T L V I C L L W A L S F I S I T P V W L  180
181  Y A R L I P F P G G A V G C G I R L P N  200
201  P D T D L Y W F T L Y Q F F L A F A L P  220
221  F V V I T A A Y V R I L Q R M T S S V A  240
241  P A S Q R S I R L R T K R V T R T A I A  260
261  I C L V F F V C W A P Y Y V L Q L T Q L  280
281  S I S R P T L T F V Y L Y N A A I S L G  300
301  Y A N S C L N P F V Y I V L C E T F R K  320
321  R L V L S V K P A A Q G Q L R A V S N A  340
341  Q T A D E E R T E S K G T                353
```